

Supplemental Figure S1

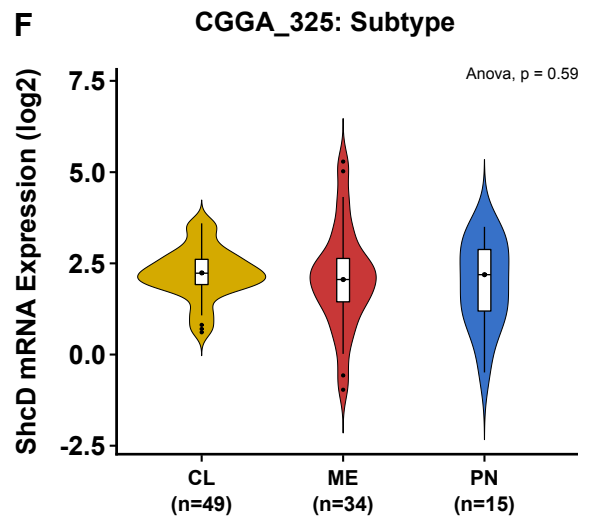
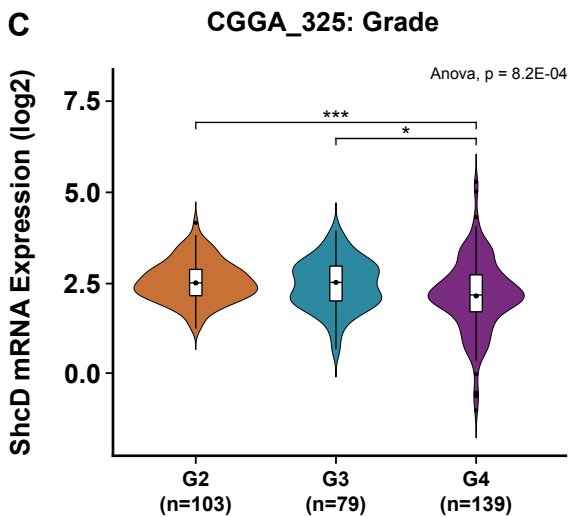
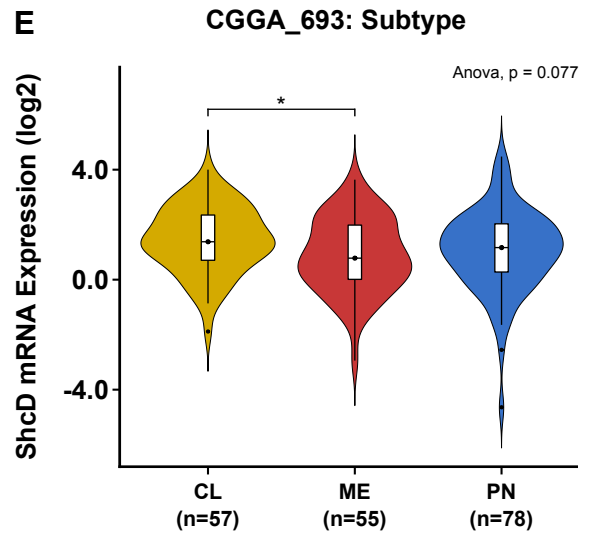
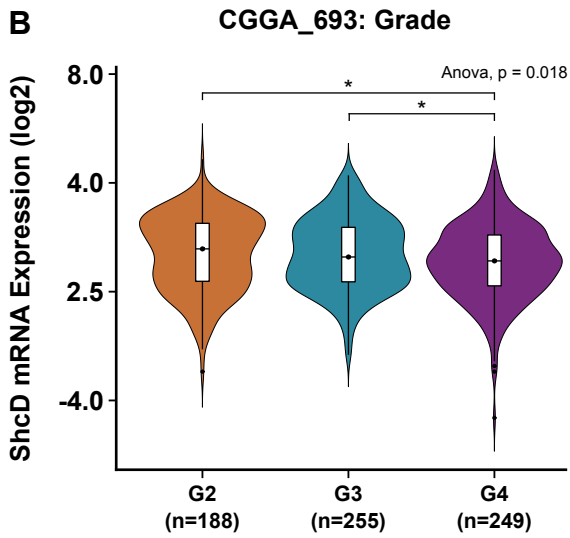
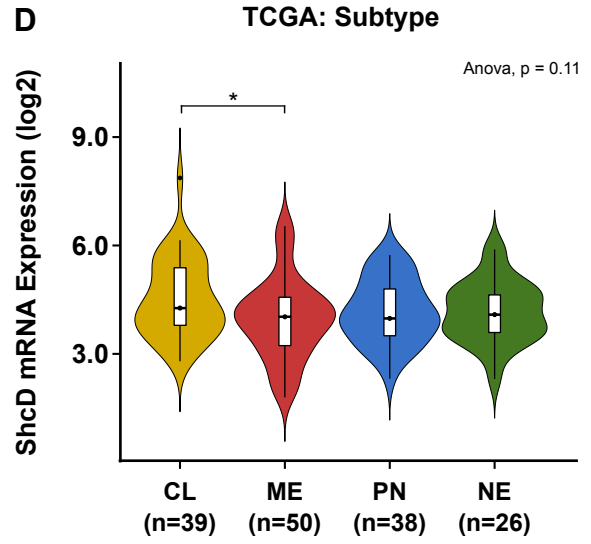
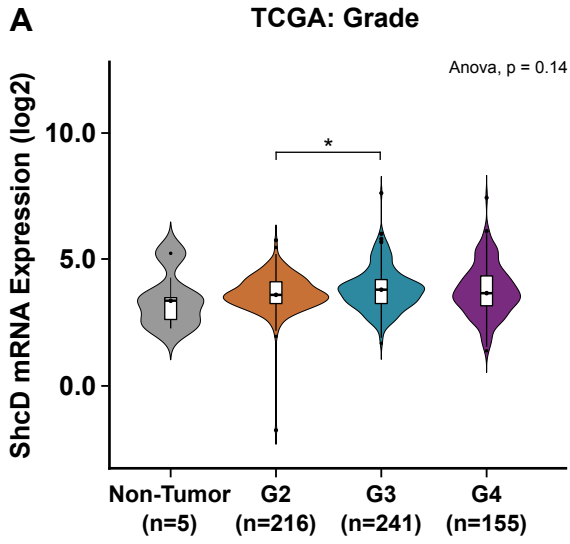


Figure S1: Bioinformatic analysis of ShcD expression in TCGA and CGGA datasets. (A-C) ShcD mRNA expression by tumor grade in TCGA-GBM+LGG (A), CGGA_693 (B) and CGGA_325 (C) datasets: violin plots depicting ShcD between non-tumoral (A only), Grade 2 (G2), Grade 3 (G3), and Grade 4 (G4) gliomas. (D-F) ShcD mRNA expression by GBM subtype in TCGA-GBM (D), CGGA_693 (E) and CGGA_325 (F) datasets: violin plots comparing ShcD expression across molecular subtypes originally reported by Verhaak *et al.* (40): Classical (CL), Mesenchymal (ME), Proneural (PN), and Neural (NE) (D only). *P*-values indicate significance levels from Kruskal-Wallis ANOVA followed by Tukey's HSD. TCGA: The Cancer Genome Atlas; GBM: Glioblastoma multiforme; LGG: Lower grade glioma; CGGA: Chinese Glioma Genome Atlas. **P* < 0.05; *** *P* < 0.001.